

Figure 1.

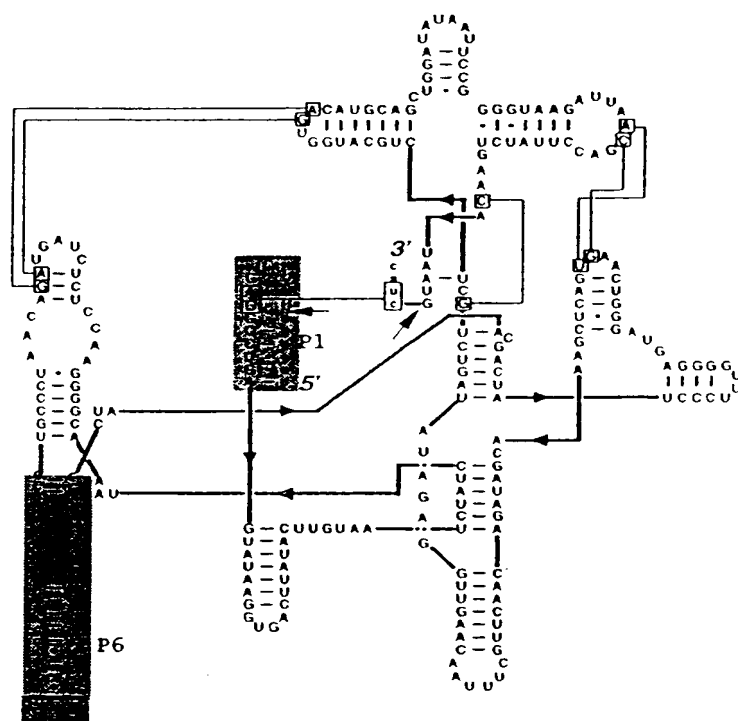
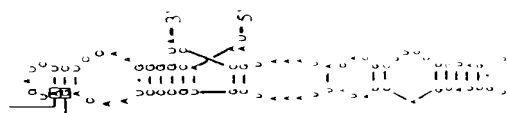
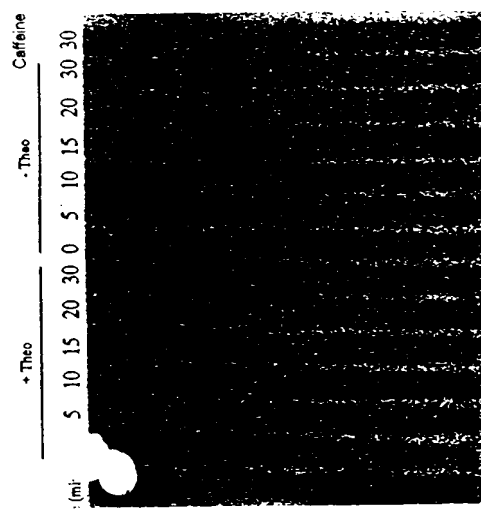
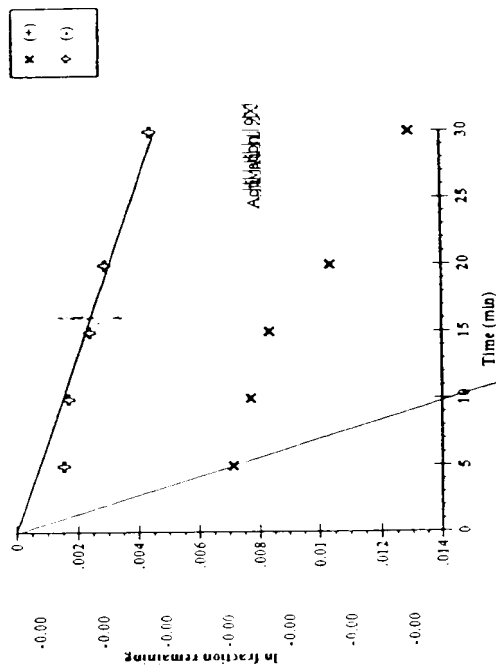


Figure 2a.

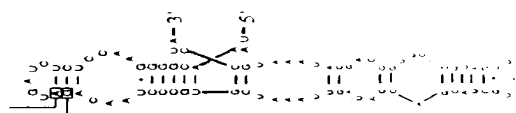
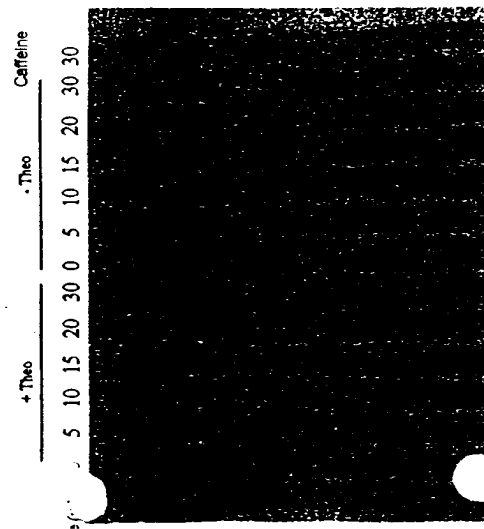


GpITH1P6.121

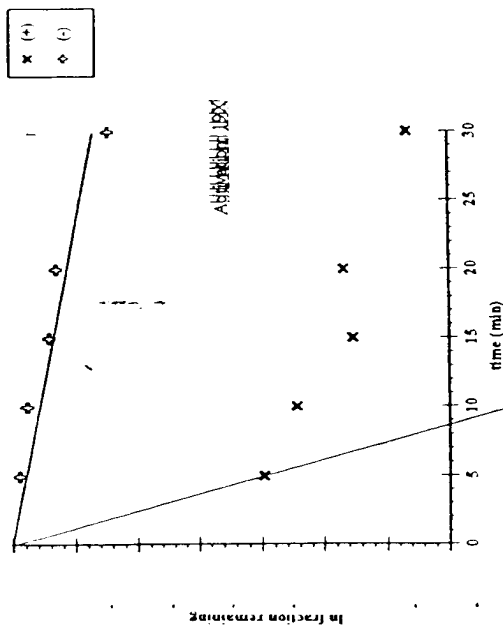


x (+)
o (-)

Figure 2b.



GP1H286.123



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Figure 3.

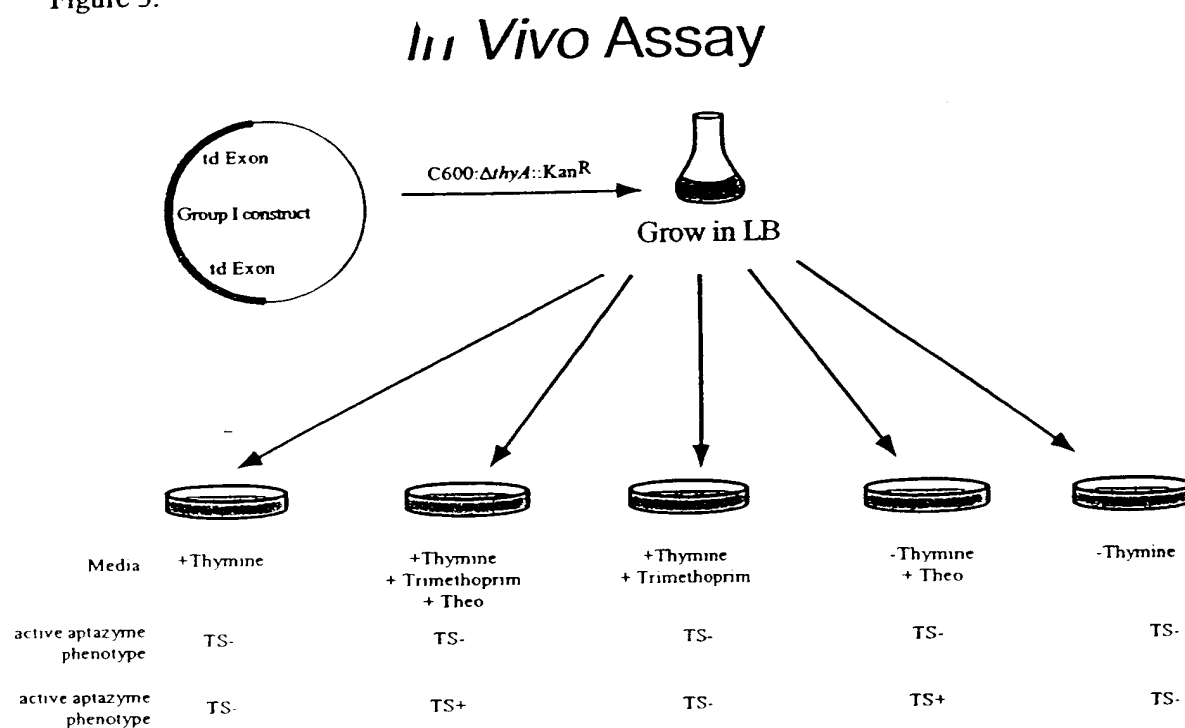
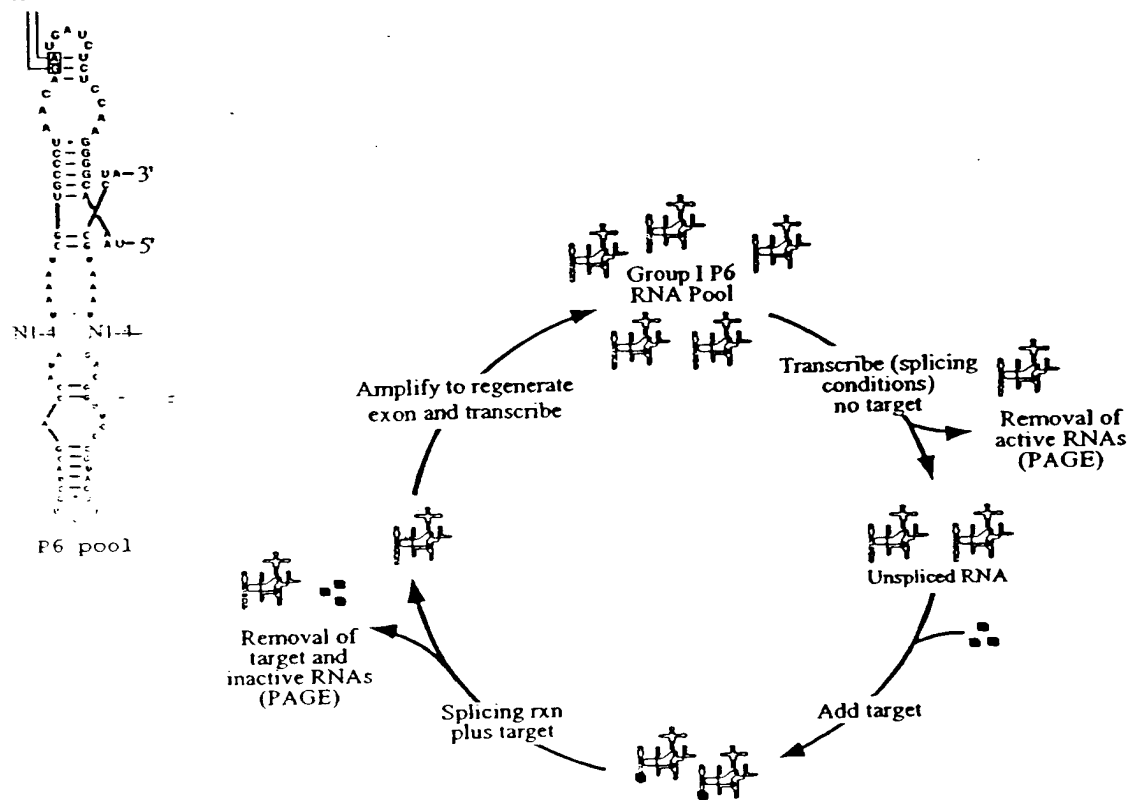


Figure 4.



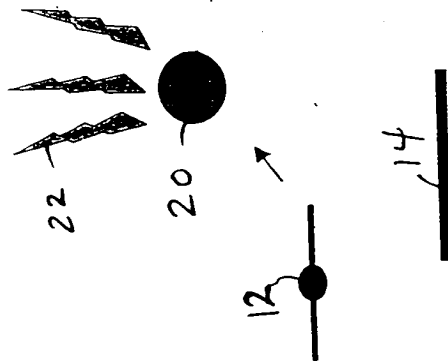
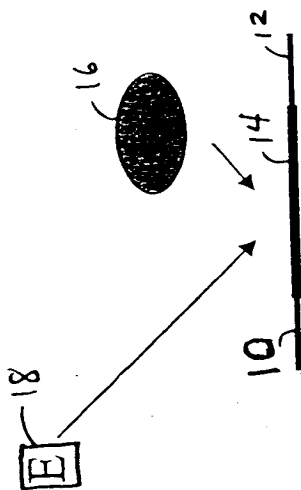


Fig. 5

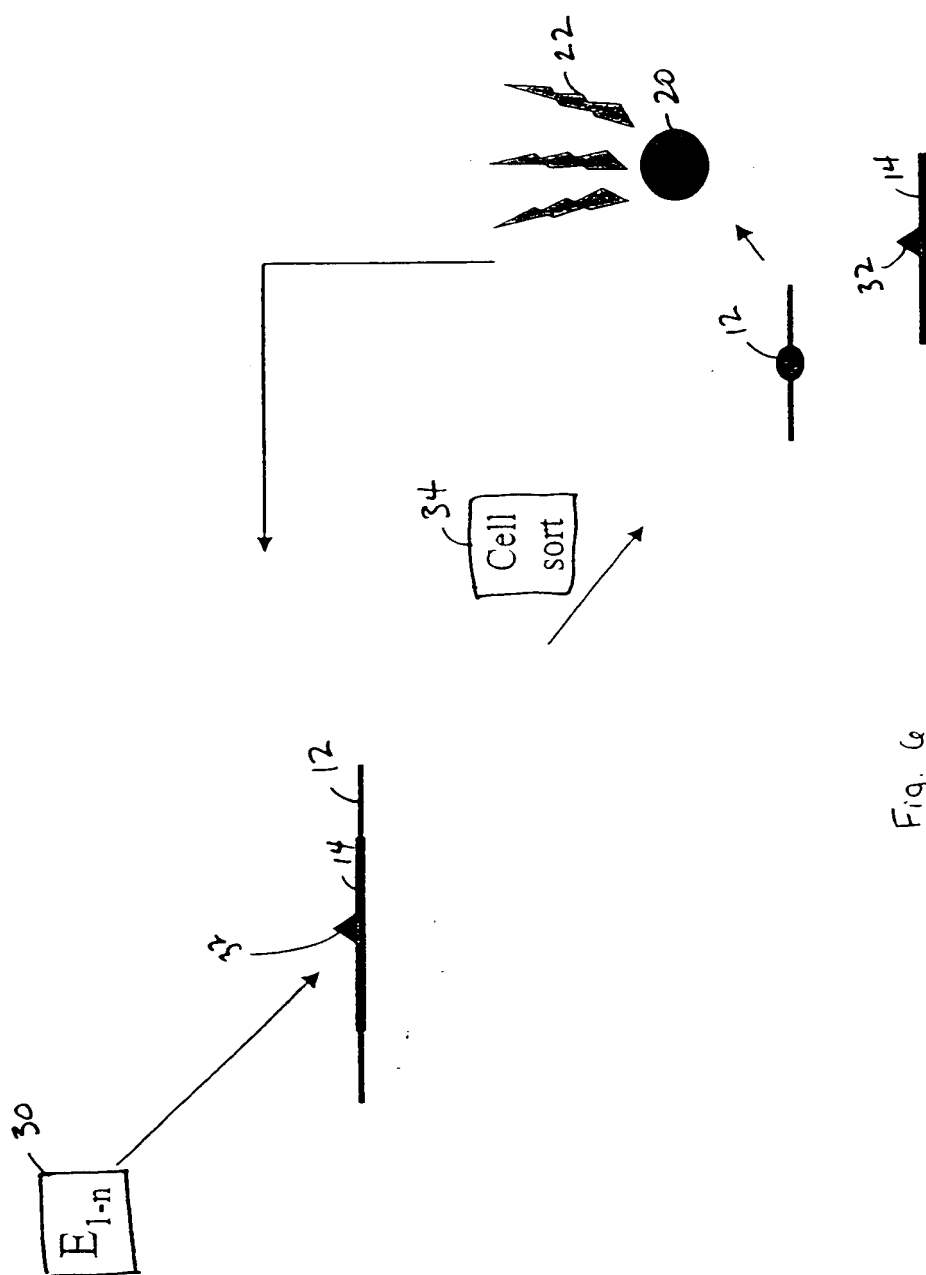


Fig. 6

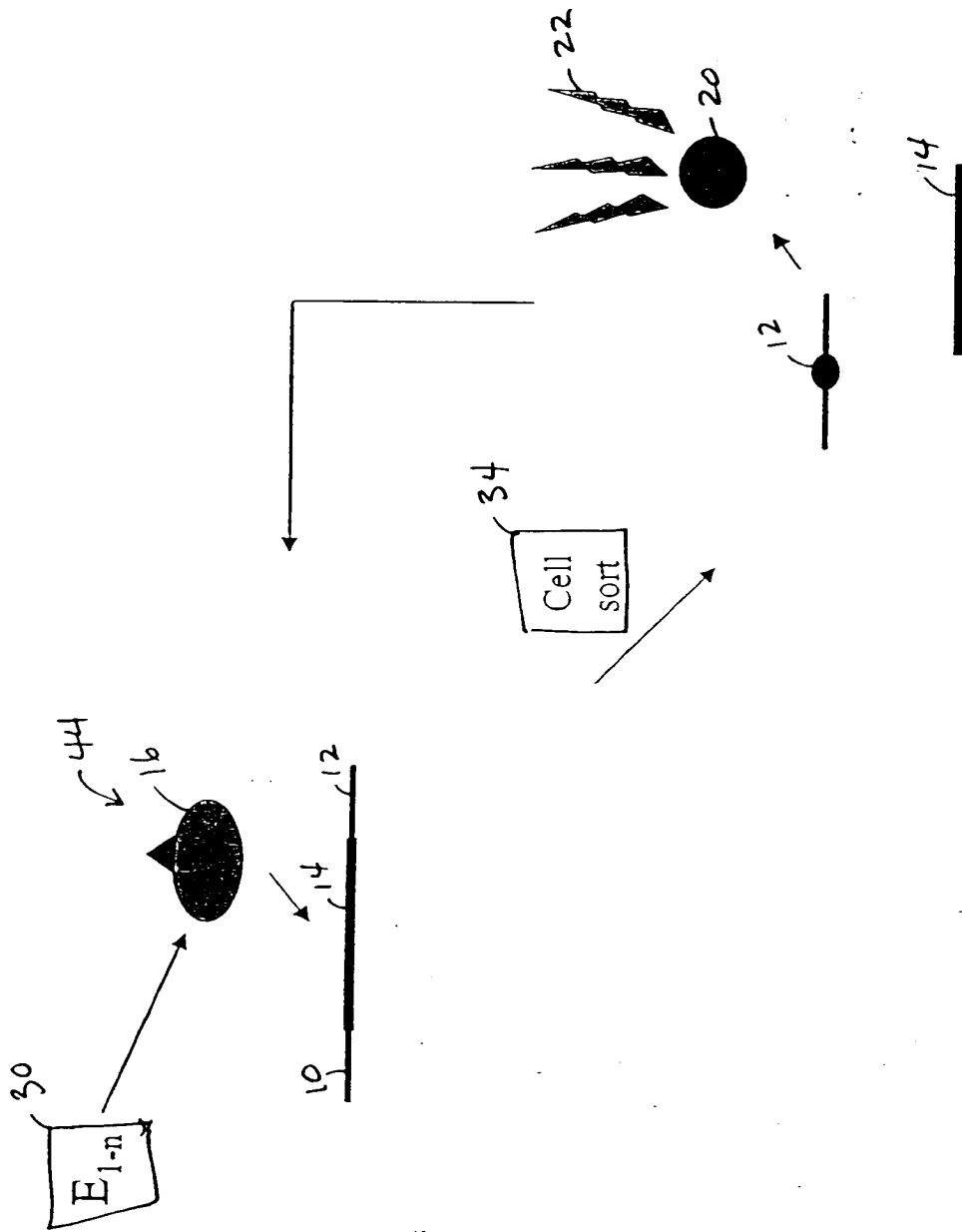


Fig. 8

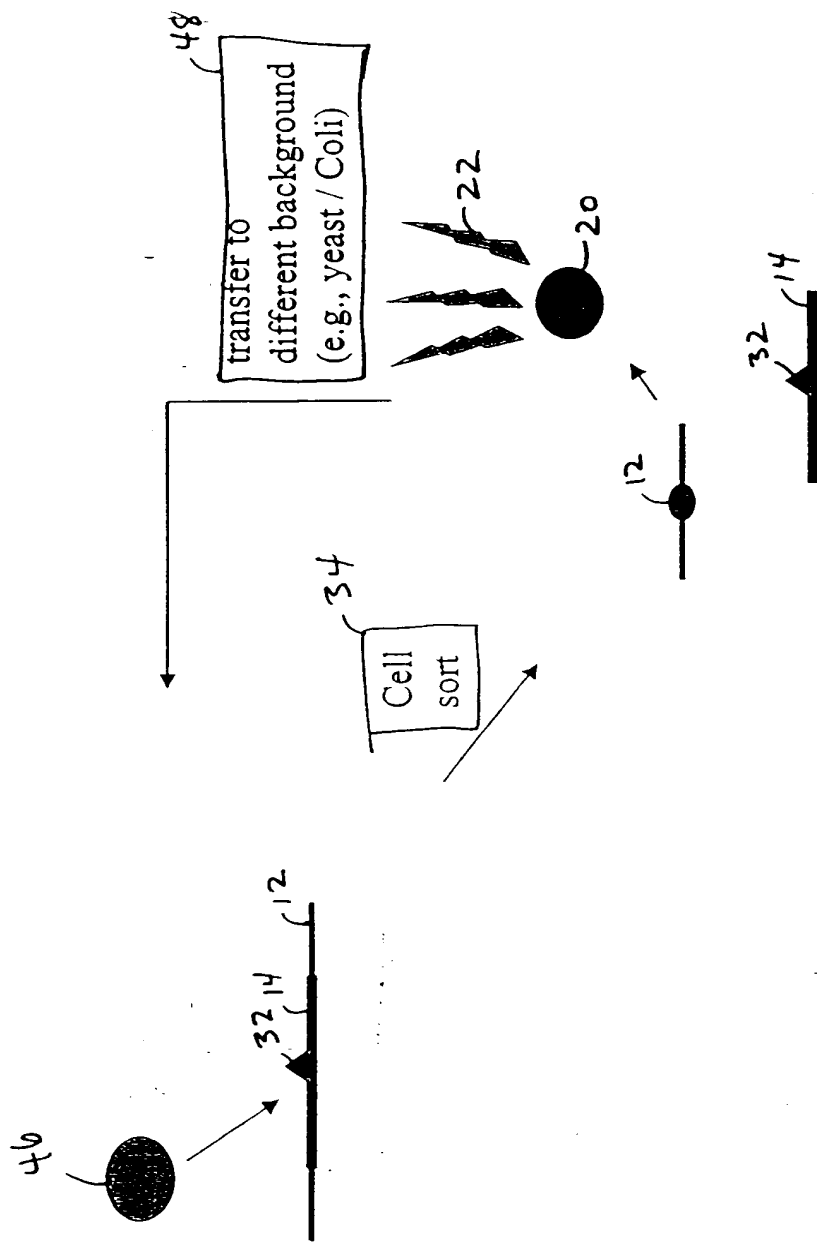


Fig. 9

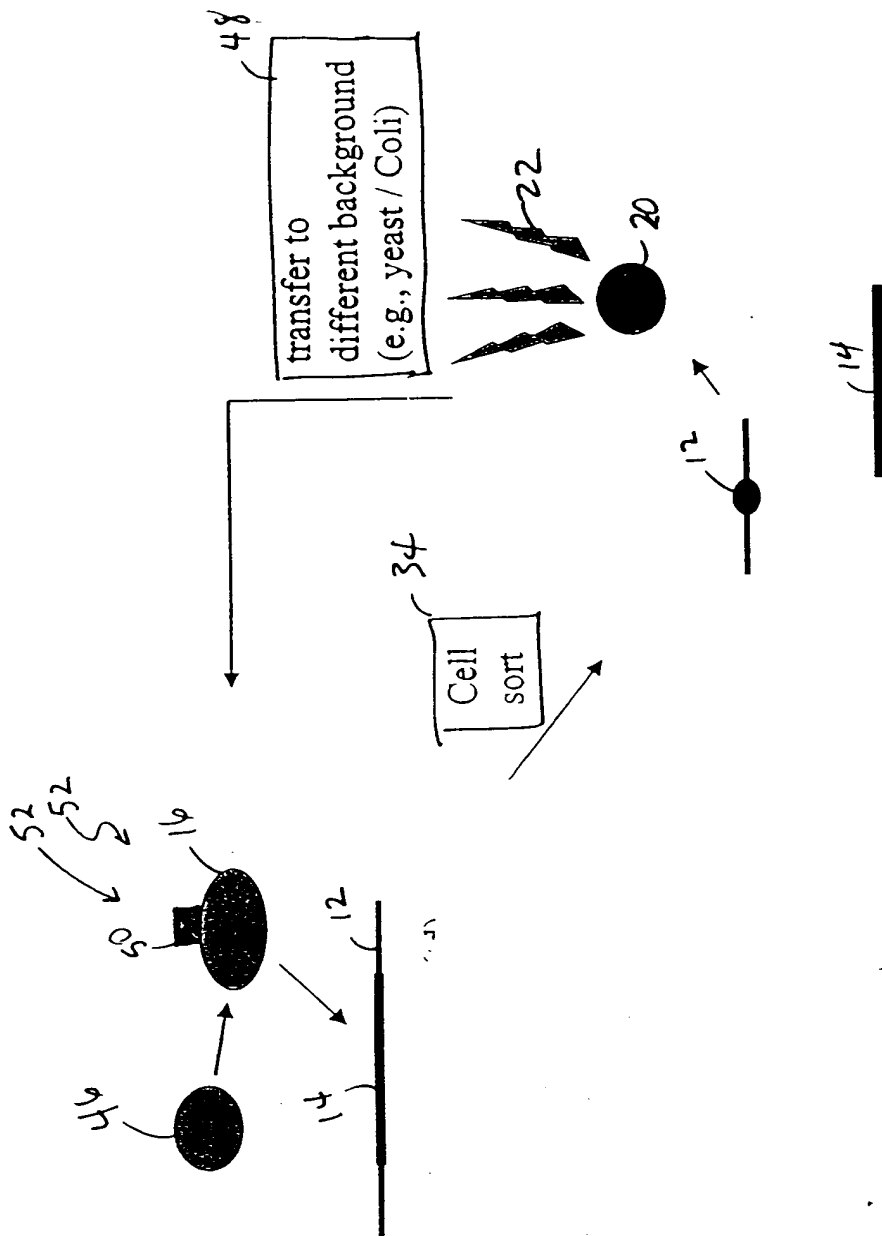


Fig. 10

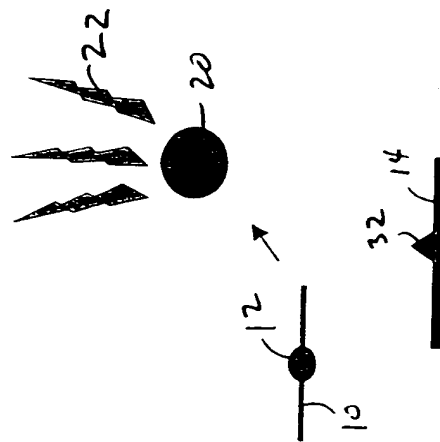
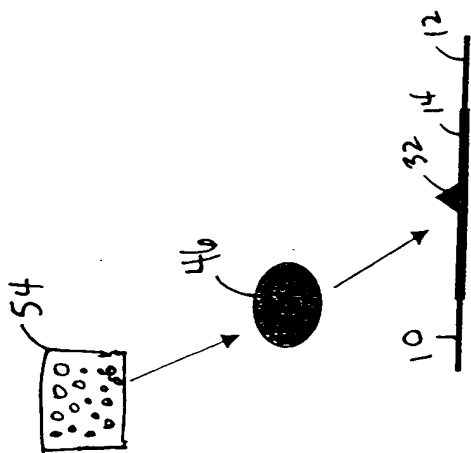


Fig. 11

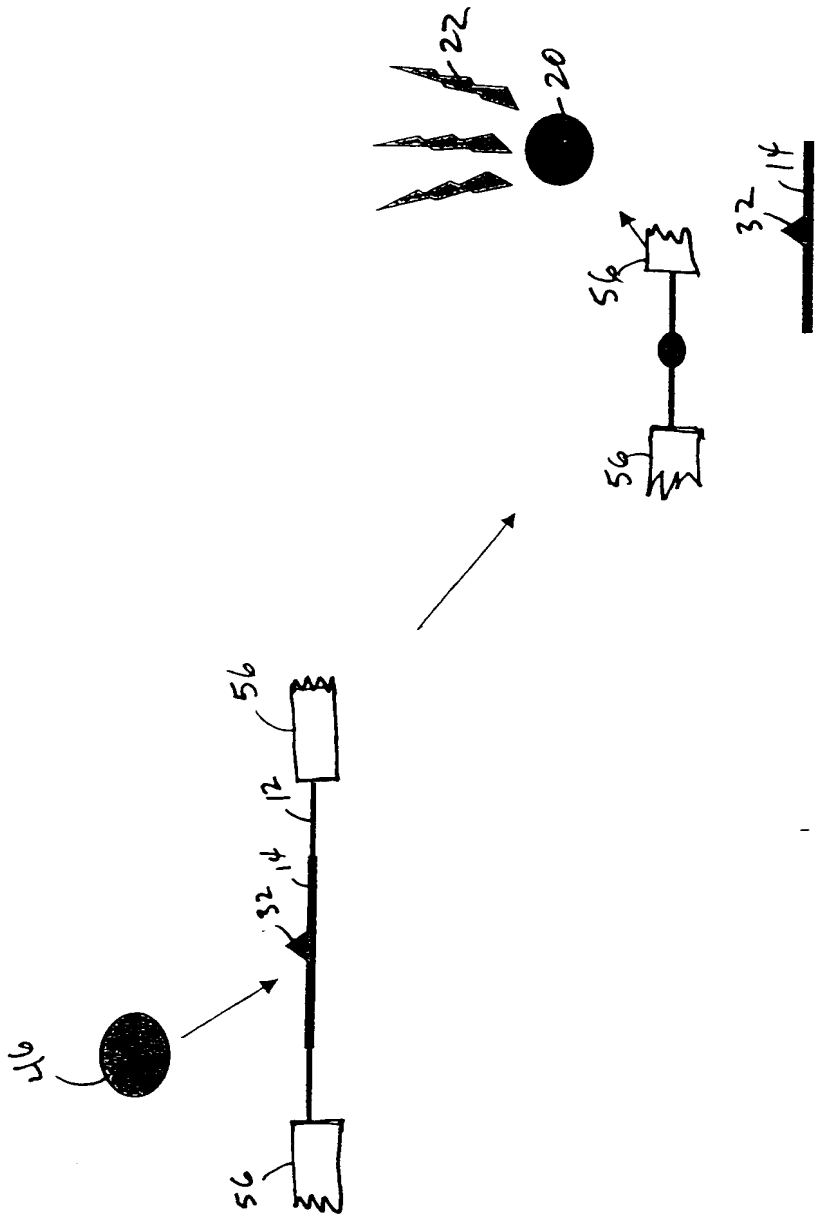


Fig. 12

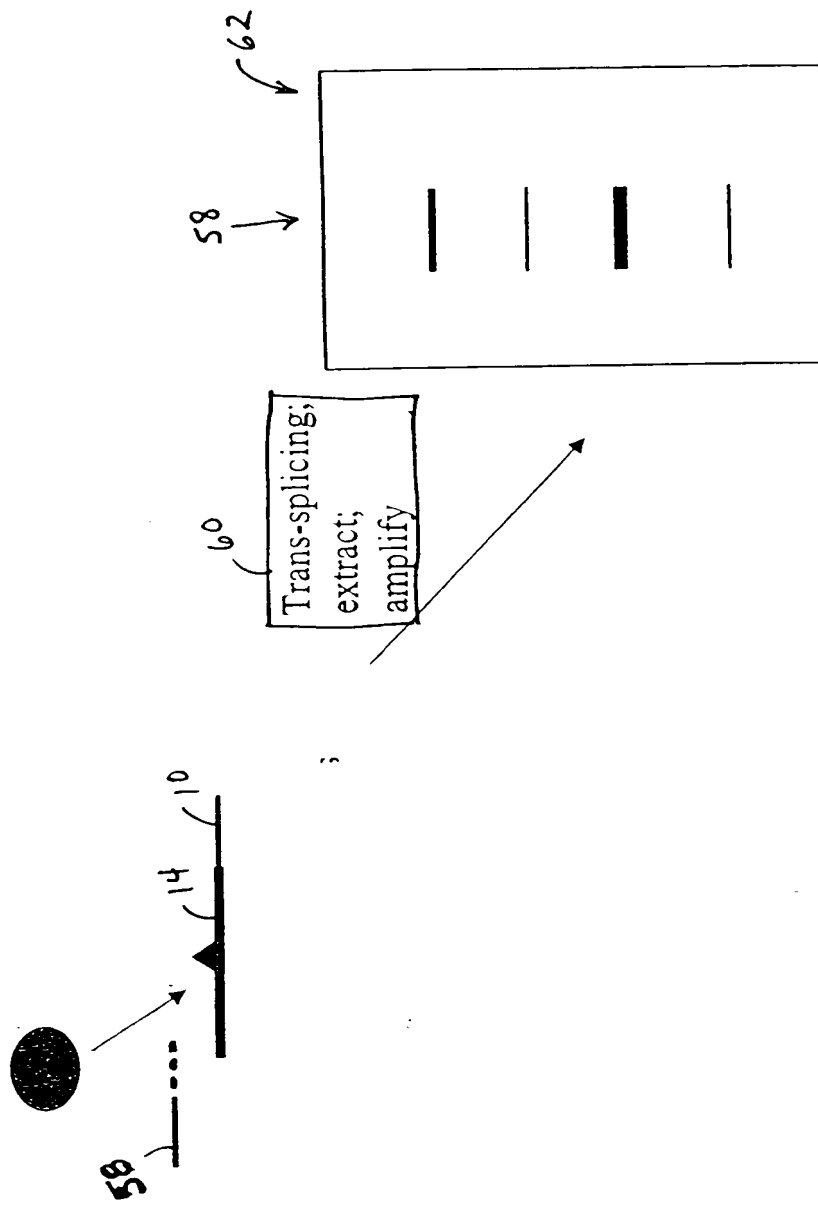


Fig. 13

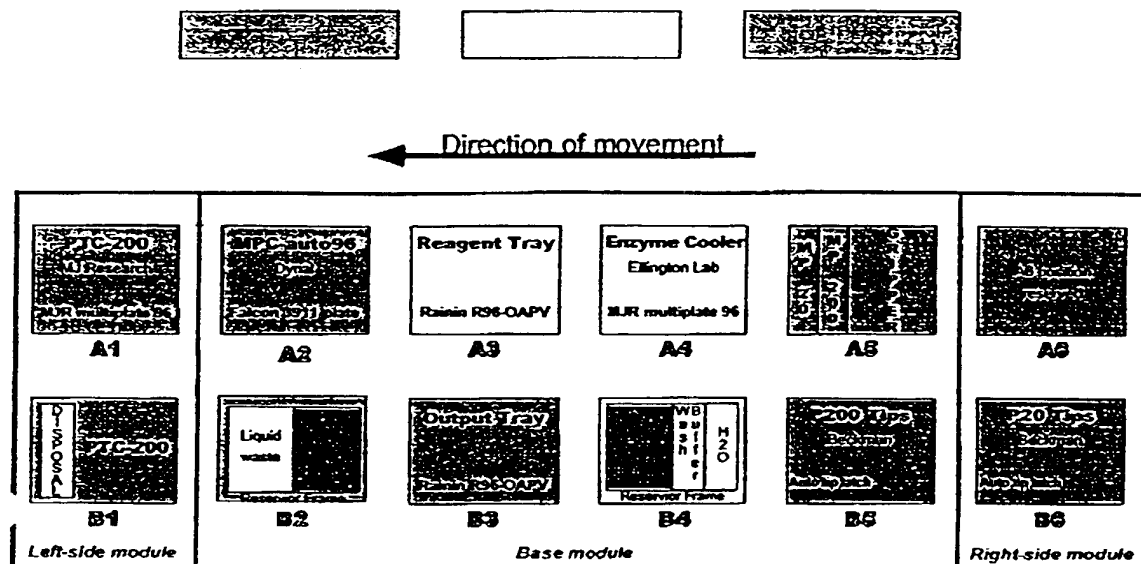


Fig. 14

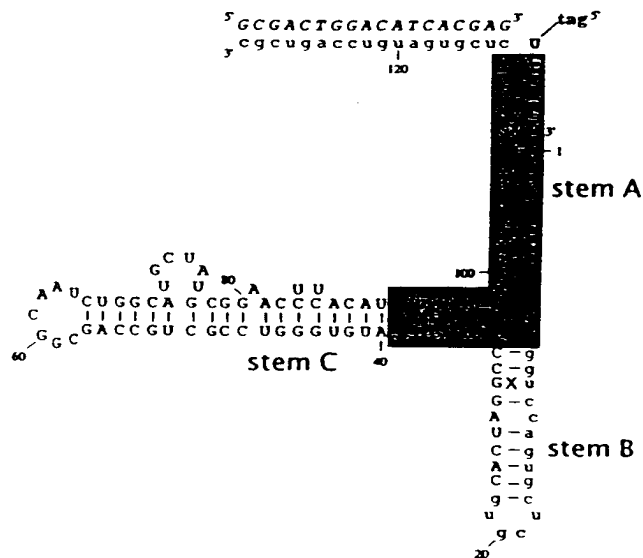


Fig. 15a

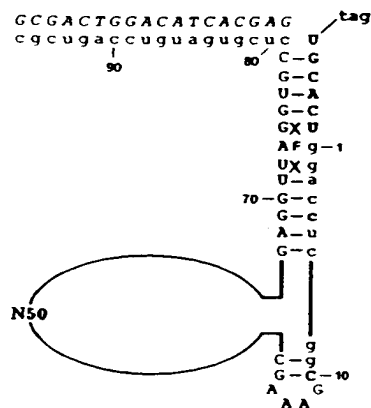


Fig. 15b

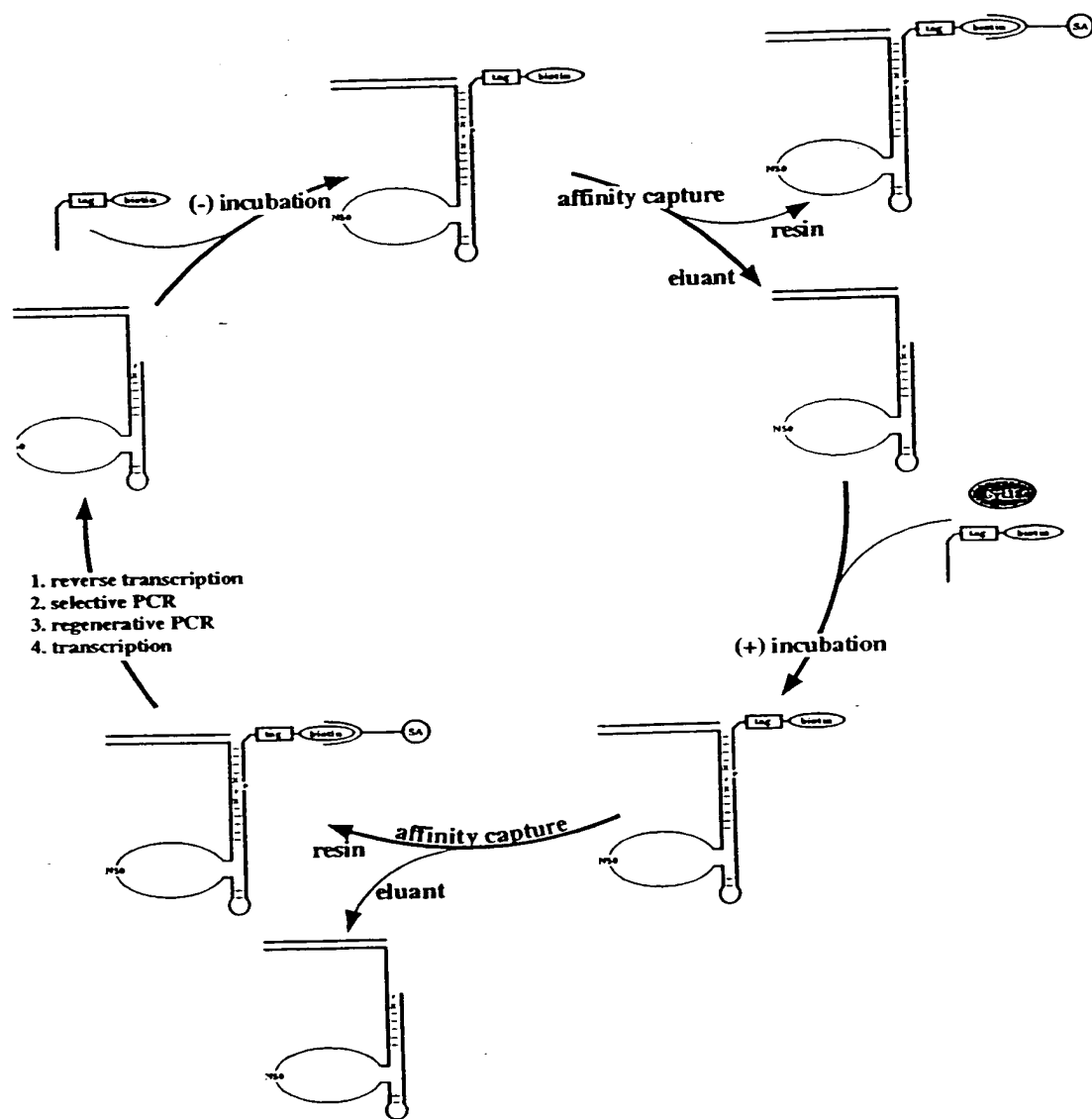


Fig. 15 c

Fig 16a

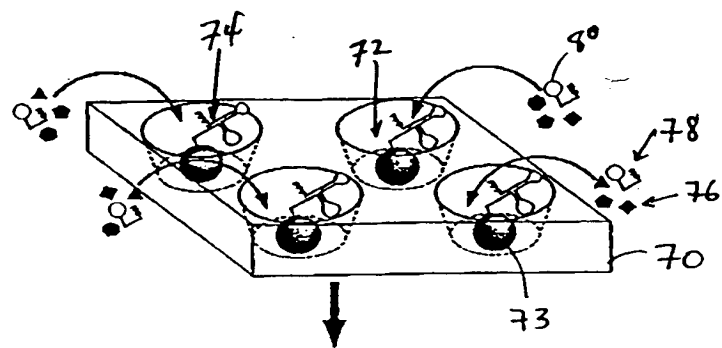


Fig 16b

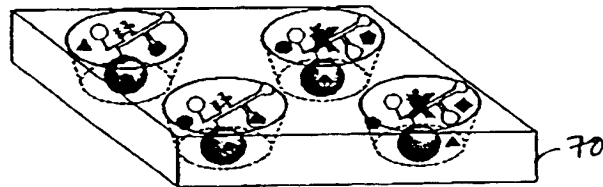


Fig 16c

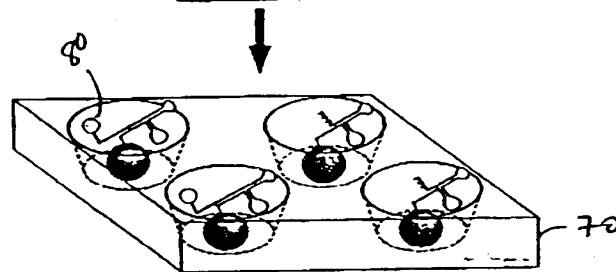


Figure 17

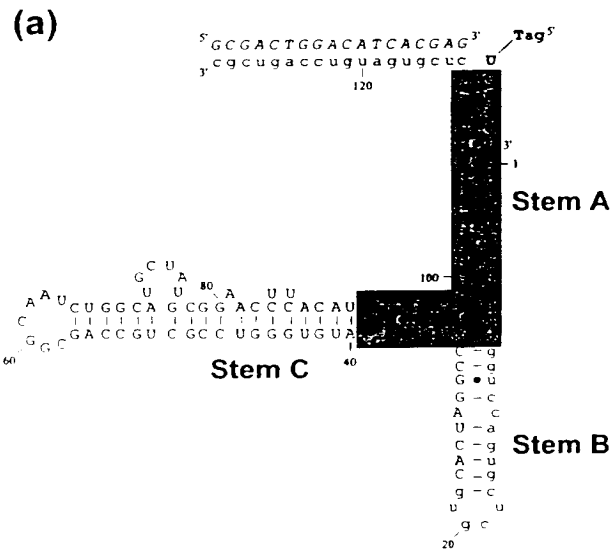


Figure 17

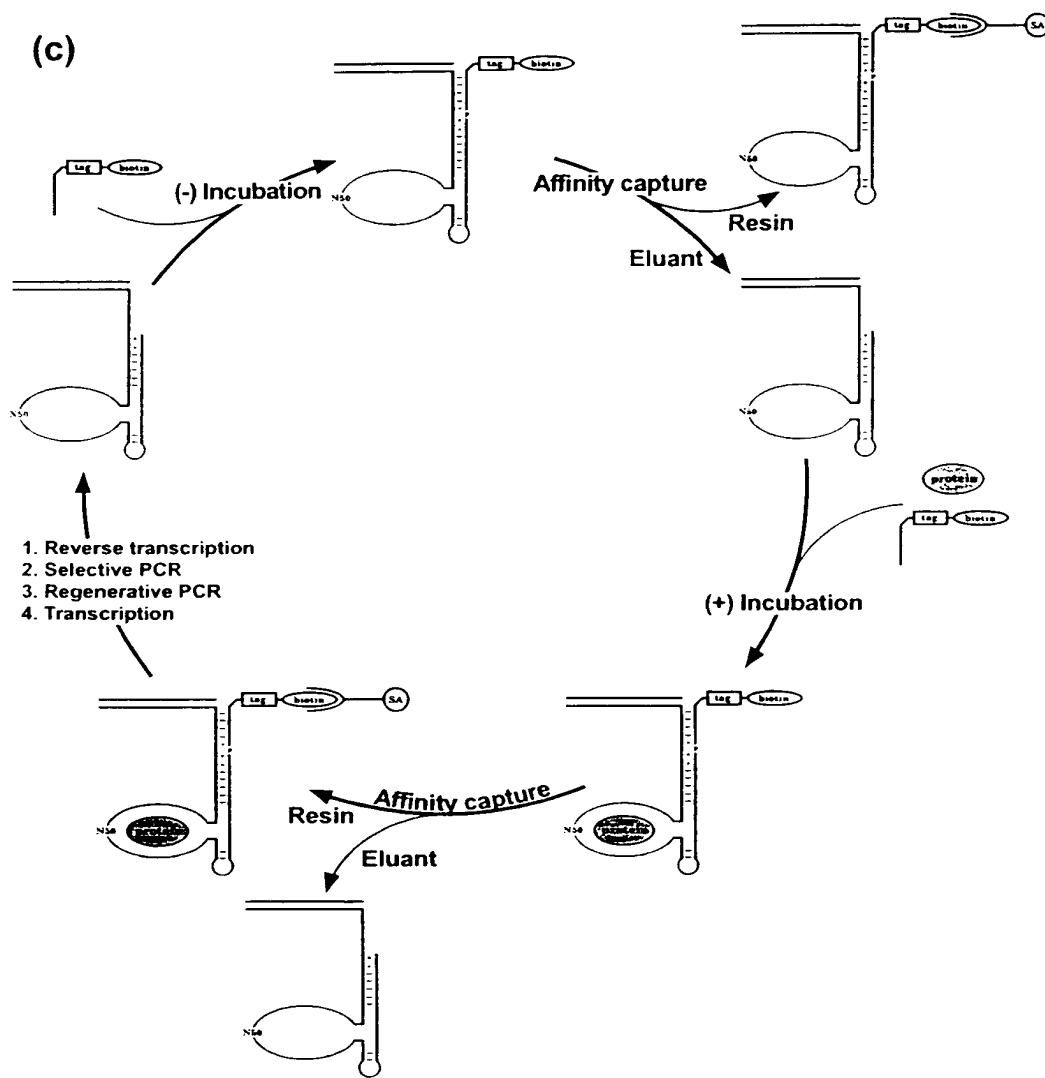


Figure 18

(a)

Round	(-) Incubation		(+) Incubation		Activation
	Substrate	(-) Cyt18	Substrate	(+) Cyt18	
1			2X	14 h	
2	2X	20 h	2X	14 h	
3	2X	20 h	2X	8 h	0.9
4	2X	20 h	2X	1 h	1.0
5	4X	44 h	2X	1 h	26
6	4X	45 h	2X	15 min	1800
7	4X	91 h	2X	5 min	61000
8			1X	30 s	66000
9	4X	20 h	1X	30 s	76000

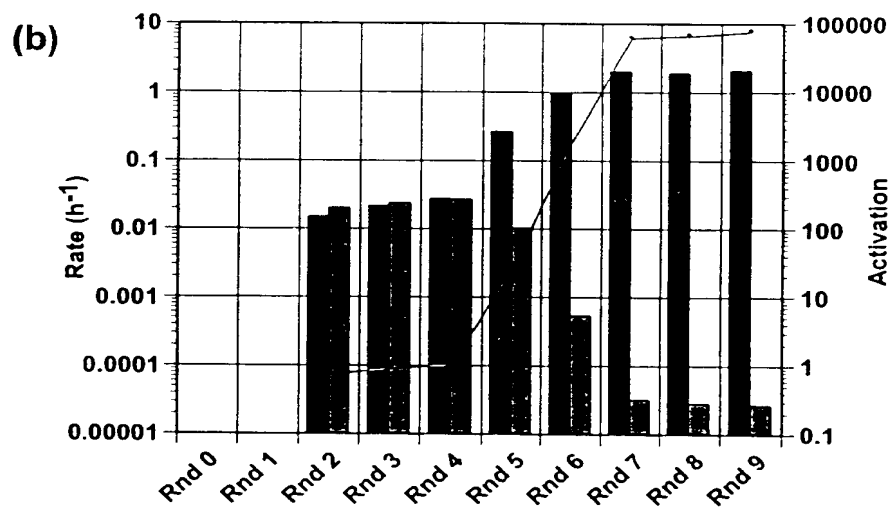


Figure 18

(c)

Round	(-) Incubation		(+) Incubation		Activation
	Substrate	(-) Lys	Substrate	(+) Lys	
1			2X	16 h	
2	2X	22 h	2X	14 h	1.0
3	2X	20 h	2X	8 h	1.0
4	2X	18 h	2X	1 h	1.0
5	4X	44 h	2X	1 h	1.0
6	4X	44 h	2X	15 min	1.7
7	4X	90 h	2X	15 min	5.0
8	4X	93 h	2X	5 min	270
9	4X	92 h	2X	1 min	630
10			1X	30 s	780
11	4X	118 h	1X	30 s	820

(d)

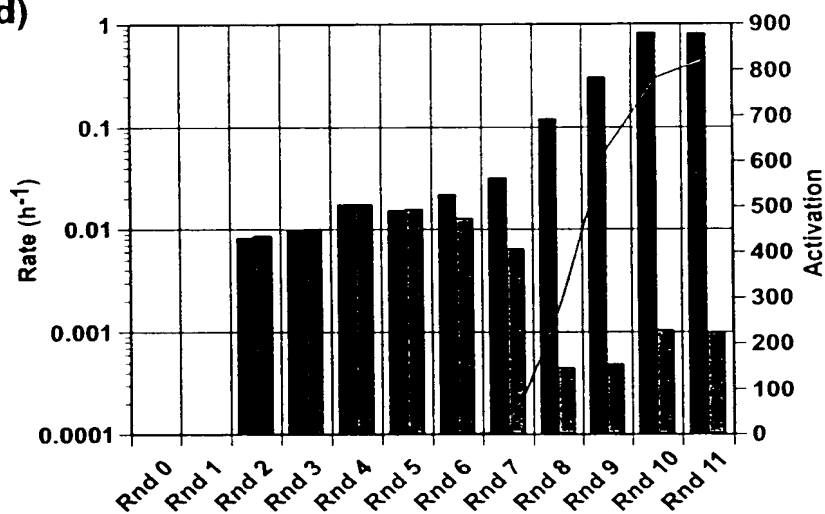


Figure 19

(a)

cyt7-2	(0.61)	CGGAAGCAAGGAGAGACGTCCTTGGAGGAGCAAGGG-----GTCTTACAGTCAGT
cyt7-6	(0.22)	CAGAGCATTAAAG---ACGGGTGACTCTTTAGTTAGGCTCCCETTAGTCTTAGG
cyt7-1	(0.08)	CAGAGCATGAAGCGGCCACGGGTGGATGTTGCCCTTG-----ETCAGTCTTGGG
cyt9-2	(0.03)	AGGAACCCCAGATTGTGTCGGGCTGTTATGCGTCGTTTATTGAGATTAC
cyt9-16	(0.03)	CAGTACGTTAATATCCCGGAGCTAGGTGCTTCTTGTGGACAGTTATGGG
cyt9-18	(0.03)	GCACACAGCACTATATTGCTTGGTCGGAGCGTTTCGTTTATTGAGTTTAC
lys11-2	(0.50)	TAACGTCTCATGGCTAAATTGCCATGT-TGCTACAAATGATATGACTAGA
lys11-3	(0.38)	TAACGAAGACTTTGGTGACCGGCTAGTCTTCTATTAATGAGATGACGAGA
lys11-28	(0.08)	TAACCCCCGCACTTAGGAACGGGTGCTGGA-TAAAAATGATATGACGAGA
lys11-6	(0.04)	TTTAAAACGAGAGAATTGGCAGTACCGTGCT-GGTTCGAGATAACGAGA

(b)

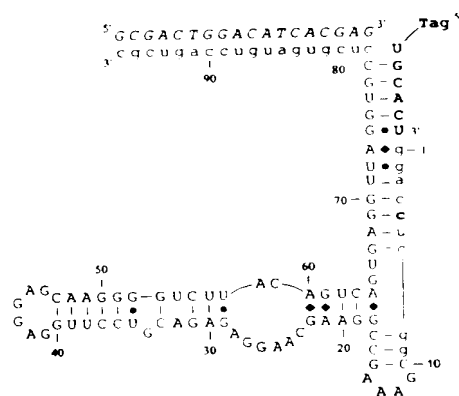


Figure 20

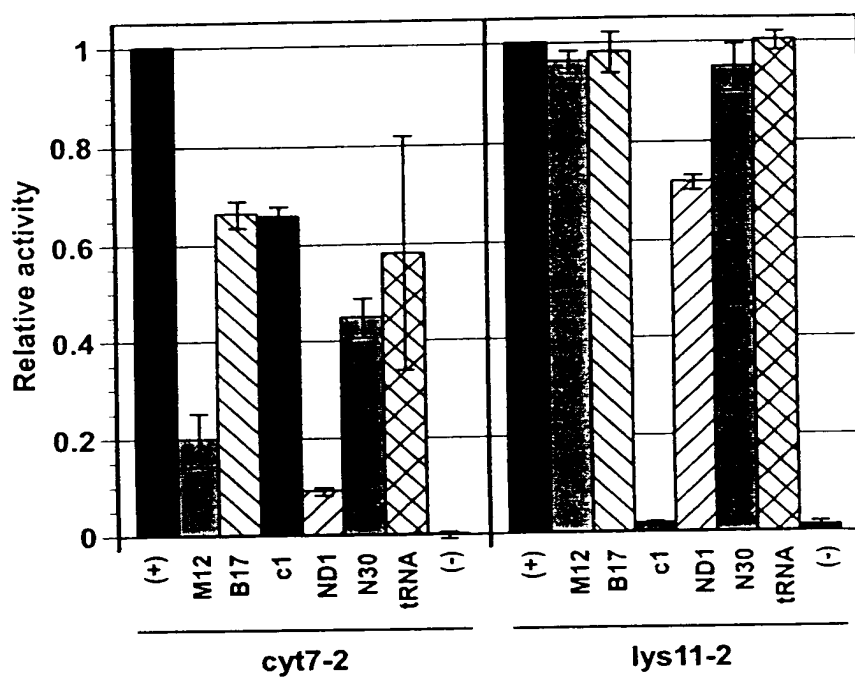


Figure 21

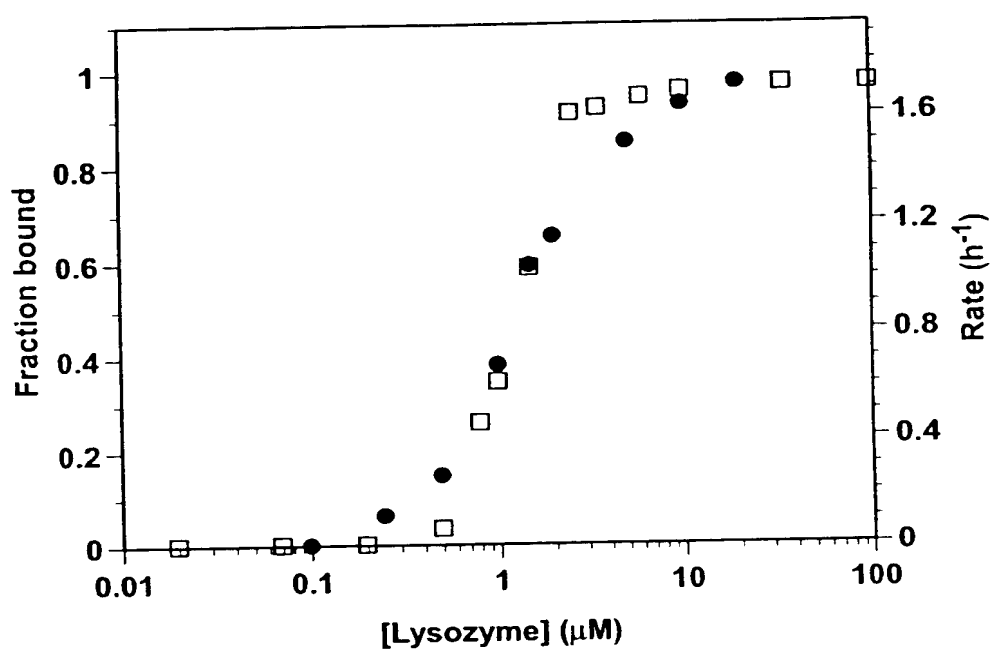


Figure 22

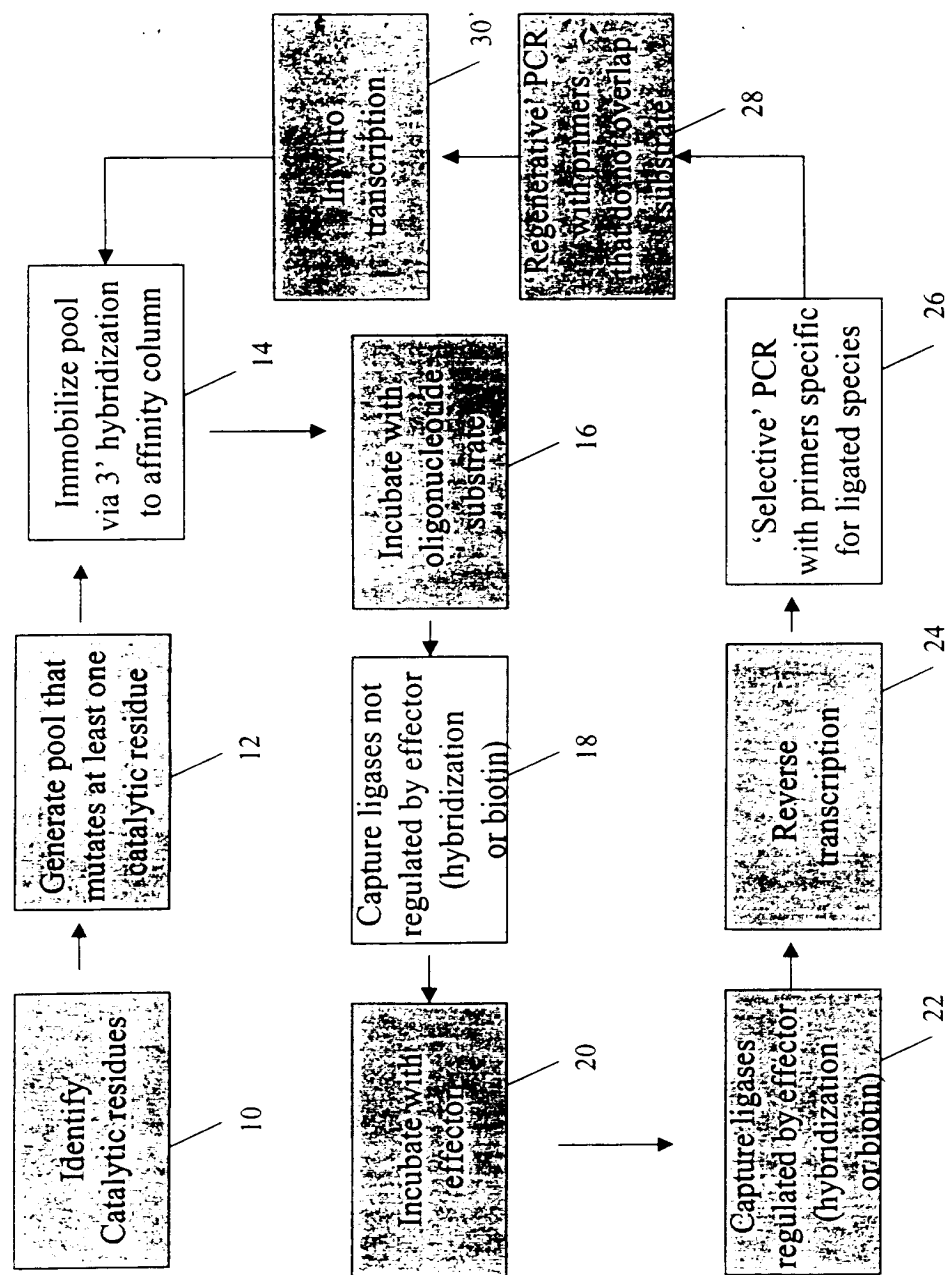


FIGURE 23

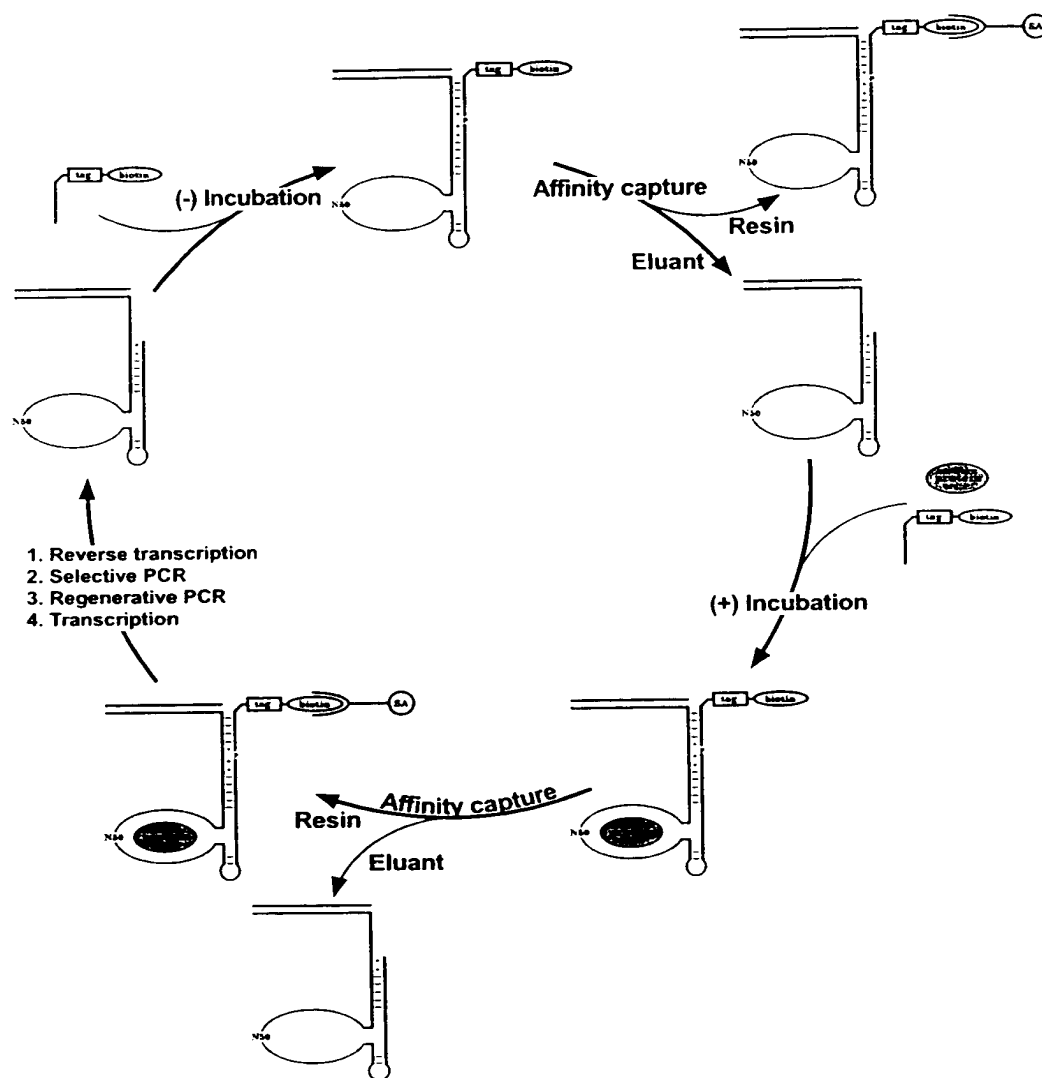


FIGURE 24

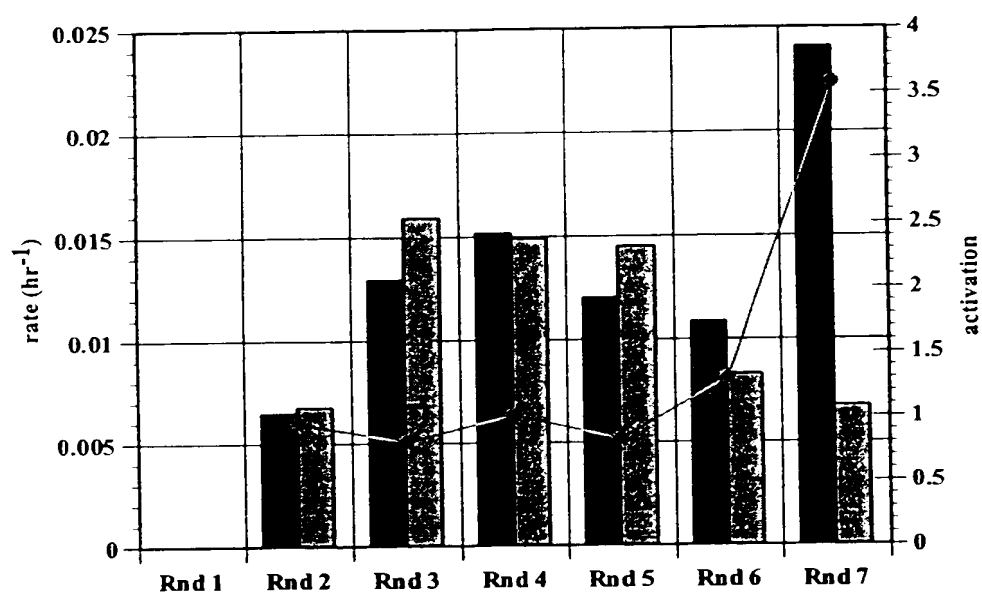
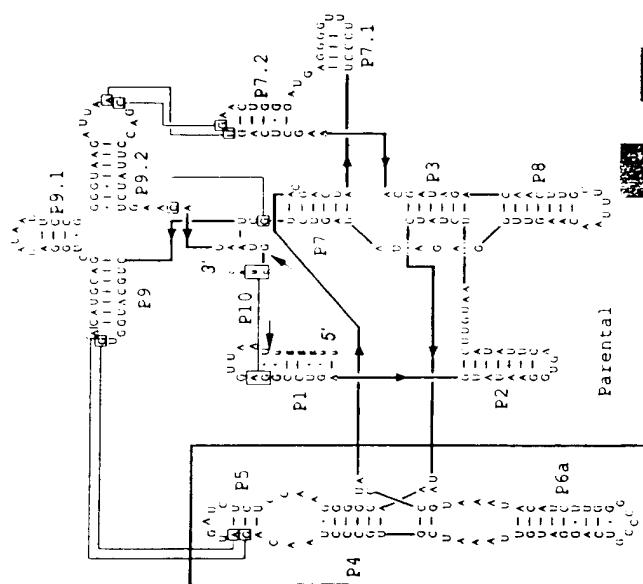
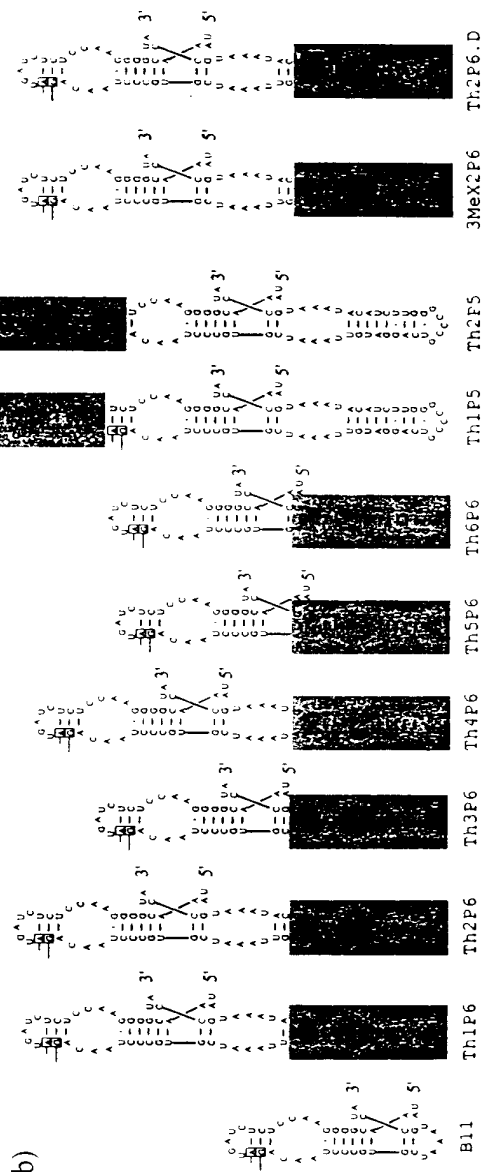


FIGURE 25

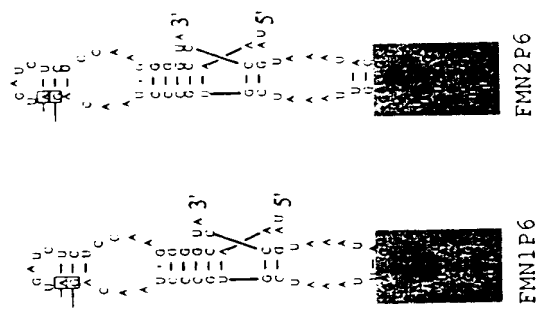


a)



b)

FIGURE 26



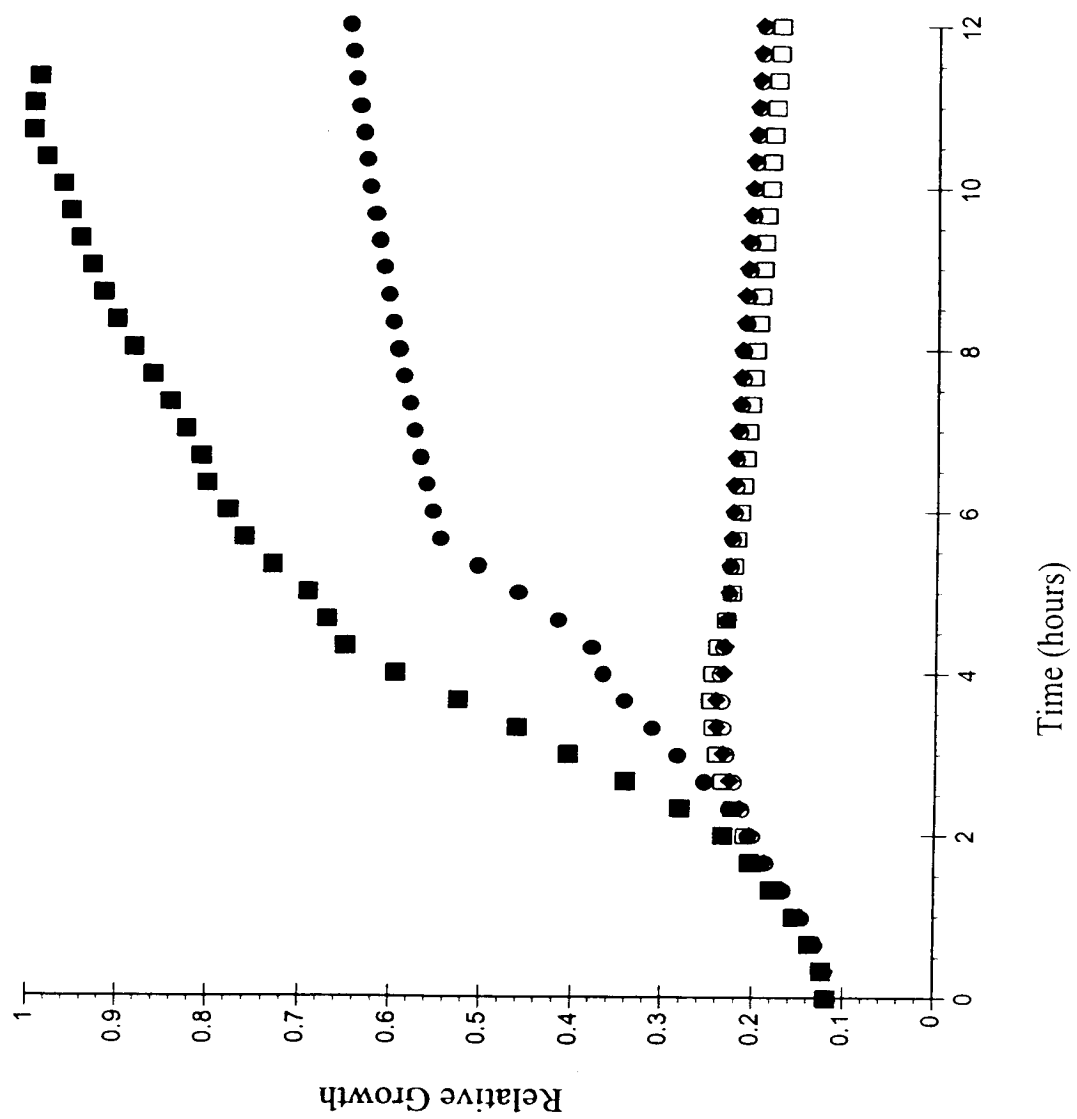


FIGURE 27(a)

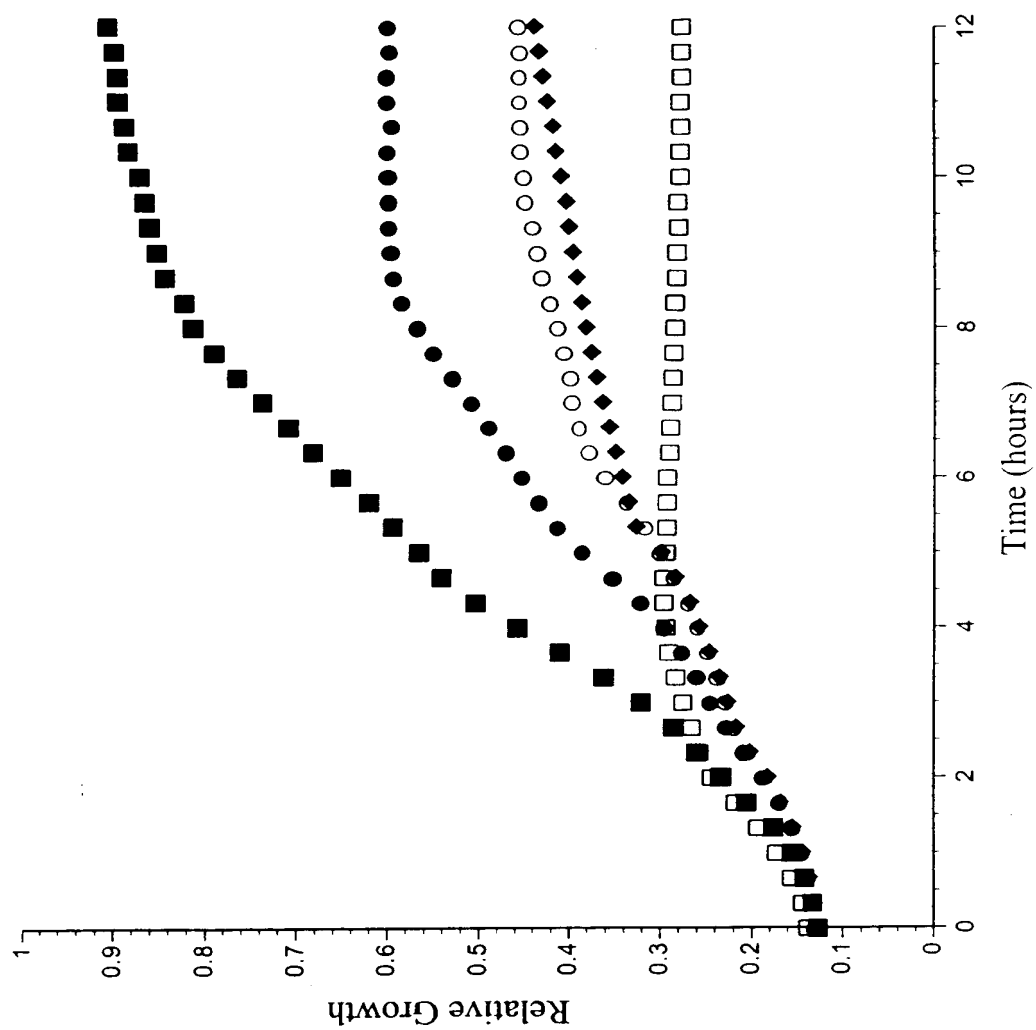


FIGURE 27(b)

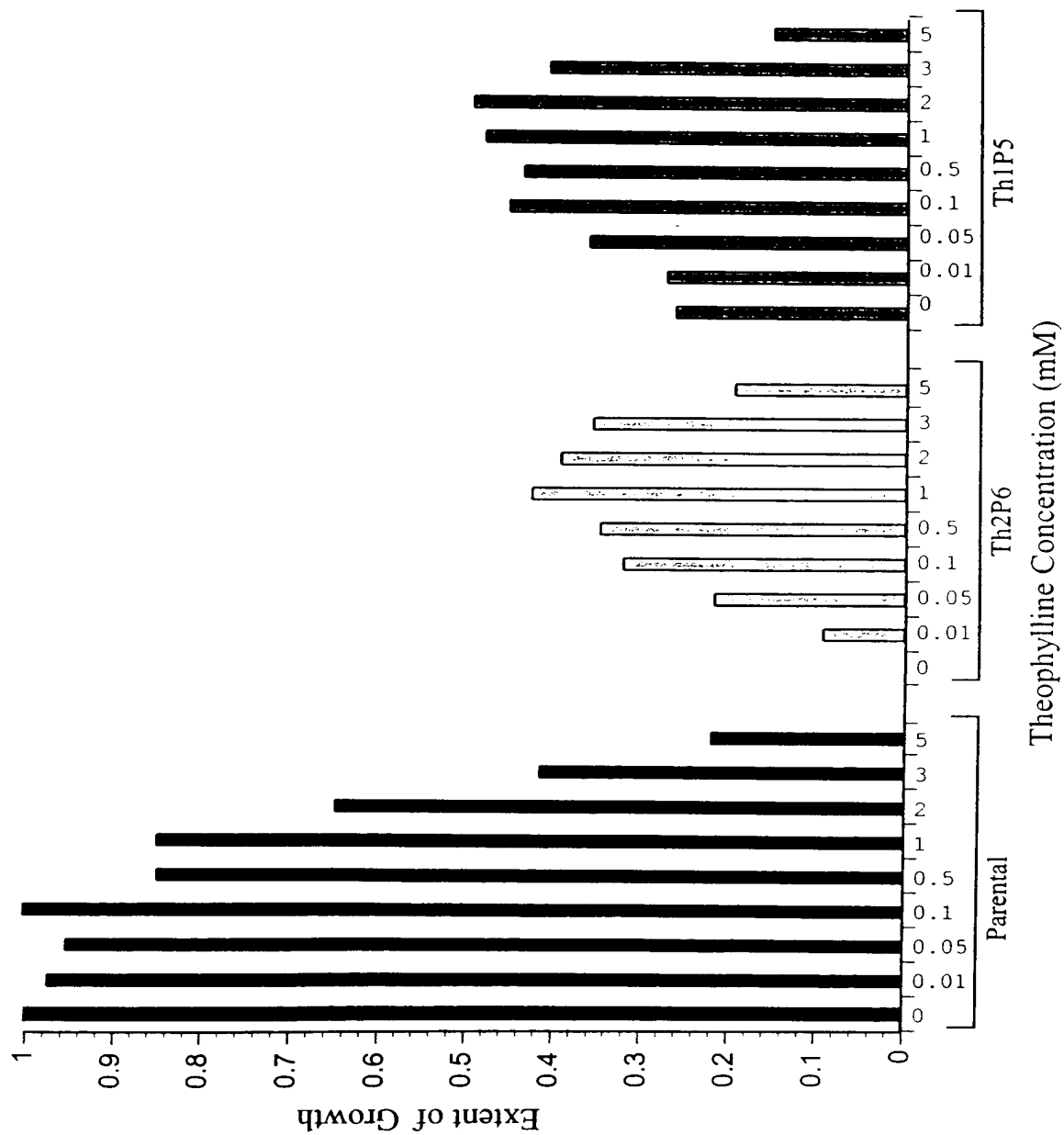


FIGURE 27(c)

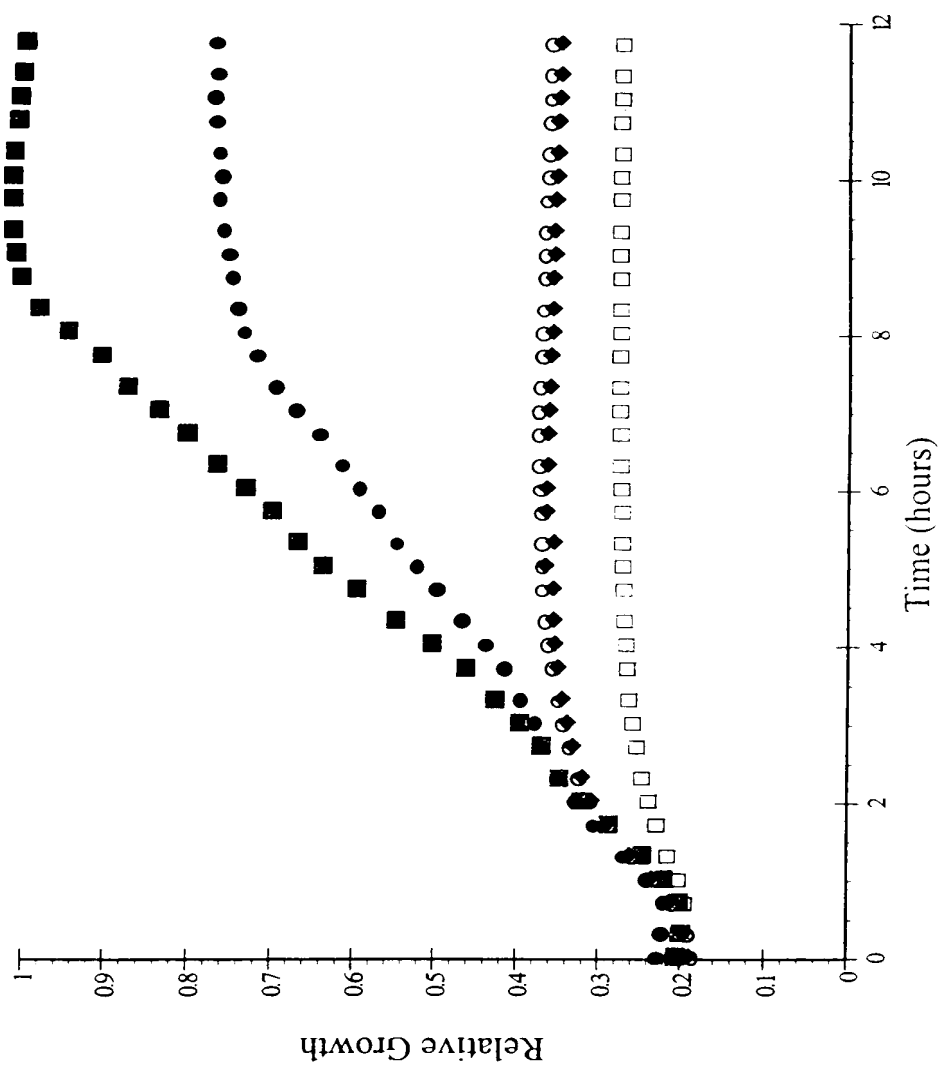
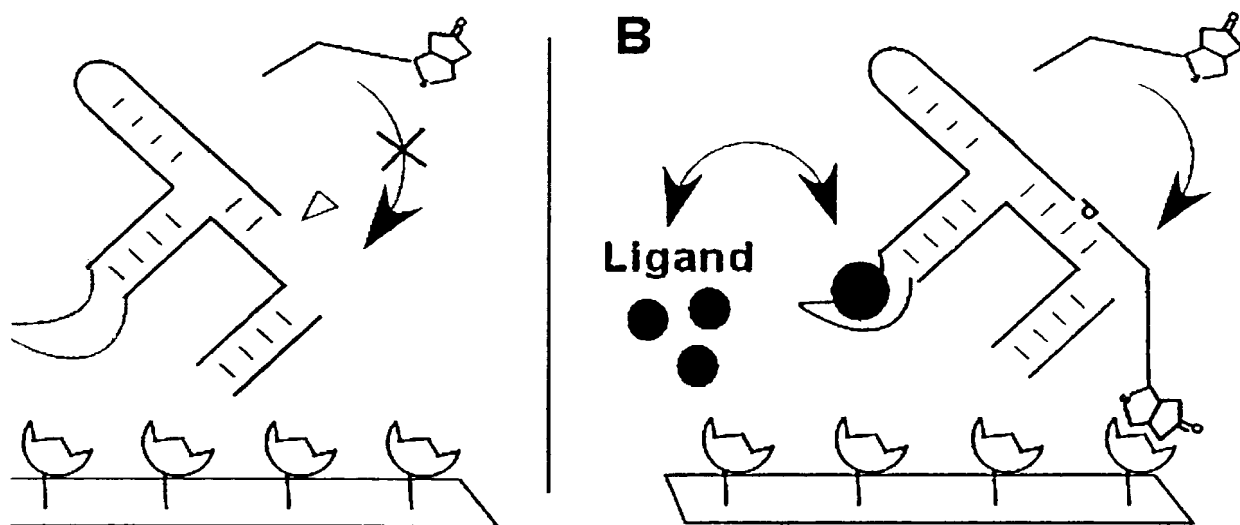


FIGURE 28

FIGURE 29



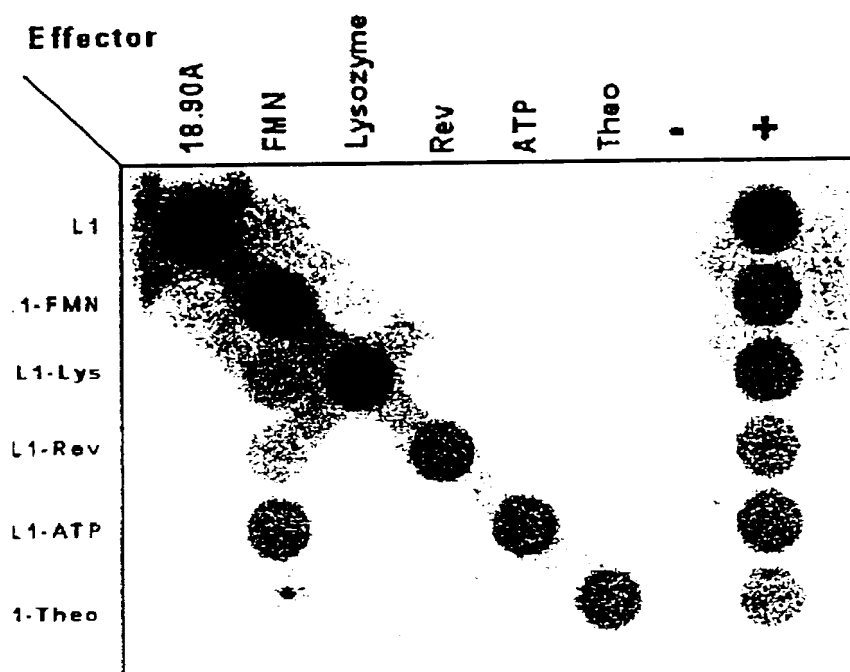
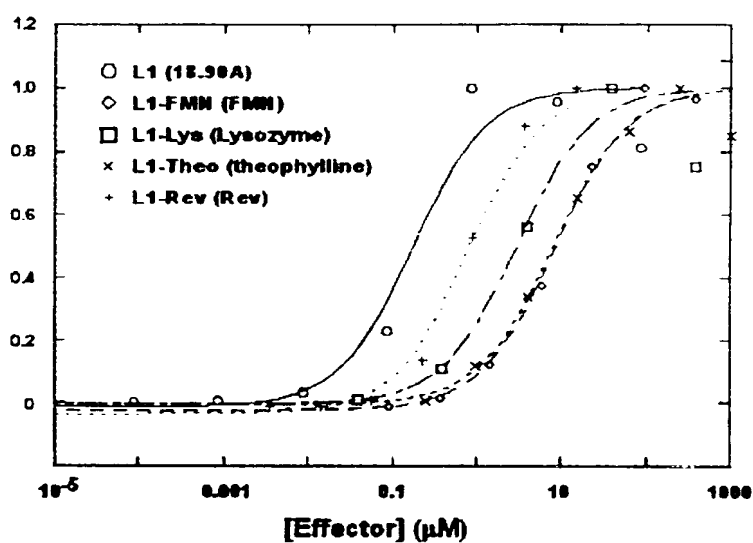


FIGURE 30

FIGURE 31



<u>Rz</u>	<u>K_d (μM)</u>	<u>% Bound (max)</u>
L1	0.16	16.5
L1-FMN	7.96	14.0
L1-Lys	2.13	22.7
L1-Theo	8.02	3.48
L1-Rev	0.77	19.0